

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/579,693
Source: IFWP
Date Processed by STIC: 5/31/06

ENTERED



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/579,693

DATE: 05/31/2006

TIME: 13:29:04

Input Set : E:\seqlist.txt
 Output Set: N:\CRF4\05312006\J579693.raw

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4 <110> APPLICANT: BASF AKTIENGESELLSCHAFT et al.
6 <120> TITLE OF INVENTION: METHODS FOR THE PREPARATION OF A FINE
7      CHEMICAL BY FERMENTATION
10 <130> FILE REFERENCE: BGI-159PC2
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/579,693
C--> 13 <141> CURRENT FILING DATE: 2006-05-18
15 <150> PRIOR APPLICATION NUMBER: PCT/IB2003/006464
16 <151> PRIOR FILING DATE: 2003-12-18
18 <160> NUMBER OF SEQ ID NOS: 15
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1650
24 <212> TYPE: DNA
25 <213> ORGANISM: Corynebacterium glutamicum
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (101)...(1627)
31 <400> SEQUENCE: 1
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33 aaacactgct tagtgccca atacgtcaa aaataaggcc atg aga atc tca aag 115
34                               Met Arg Ile Ser Lys
35                               1           5
37 gcc aat gcg tat gtt gca gcg att gac caa ggc acc act tcc act cgg 163
38 Ala Asn Ala Tyr Val Ala Ile Asp Gln Gly Thr Thr Ser Thr Arg
39          10          15          20
41 tgc atc ttc att gat gcc caa gga aaa gtg gtg tct tct gct tcc aag 211
42 Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val Ser Ser Ala Ser Lys
43          25          30          35
45 gag cac cgc caa atc ttc cca caa cag ggc tgg gta gag cac gat cct 259
46 Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp Val Glu His Asp Pro
47          40          45          50
49 gaa gaa att tgg gac aac att cga tct gtc agc cag gcg atg gtc 307
50 Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val Ser Gln Ala Met Val
51          55          60          65
53 tcc att gac atc acc cca cac gag gtt gca tcg ctg gga gtc acc aac 355
54 Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser Leu Gly Val Thr Asn
55          70          75          80          85
57 cag cgc gaa acc acc gtg gtg tgg gac aag cac acc ggc gaa cct gtc 403
58 Gln Arg Glu Thr Thr Val Val Trp Asp Lys His Thr Gly Glu Pro Val
59          90          95          100
61 tac aac gca atc gtg tgg caa gac acc cgc acc tct gac att tgc cta 451
62 Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr Ser Asp Ile Cys Leu
63          105         110         115

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65	gag atc gcg ggc gaa gaa ggc cag gaa aag tgg ctt gac cgc acc ggc	499
66	Glu Ile Ala Gly Glu Gly Gln Glu Lys Trp Leu Asp Arg Thr Gly	
67	120 125 130	
69	ctg ctg atc aac tcc tac cca tcg ggg ccc aaa atc aag tgg att ctc	547
70	Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys Ile Lys Trp Ile Leu	
71	135 140 145	
73	gac aac ctt gag gga gct cgc gaa cgc gcc gaa aag ggc gac ctt ttq	595
74	Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu Lys Gly Asp Leu Leu	
75	150 155 160 165	
77	ttt ggc acc atg gat acc tgg gtg ctg tgg aac ctg acc ggc ggt gtc	643
78	Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn Leu Thr Gly Gly Val	
79	170 175 180	
81	cgc ggc gac gac ggt gat gat gcc atc cac gtc acc gat gtc acc aac	691
82	Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val Thr Asp Val Thr Asn	
83	185 190 195	
85	gca tcc cgc aca cta ttg atg gat ctc cgc acg caa cag tgg gat cca	739
86	Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr Gln Gln Trp Asp Pro	
87	200 205 210	
89	gaa cta tgc taa gcc cta gac att ccg atg tcc atg ctc cct gag atz	787
90	Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser Met Leu Pro Glu Ile	
91	215 220 225	
93	cgt ccc tcc gtc gga gaa ttc cgc tcc gtg cgc cac cgc gga acc cta	835
94	Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg His Arg Gly Thr Leu	
95	230 235 240 245	
97	gcc gac gtc ccg att act ggc gtg ctc ggc gac cag caa gcg gcc ctt	883
98	Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp Gln Gln Ala Ala Leu	
99	250 255 260	
101	ttt ggt cag ggc gga ttc cac gaa ggt gct gct aaa aat acc tac ggc	931
102	Phe Gly Gln Gly Phe His Glu Gly Ala Ala Lys Asn Thr Tyr Gly	
103	265 270 275	
105	acc ggc ctc ttc ctg ctg atg aac acc ggc acc tcg ttg aag att tcc	979
106	Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr Ser Leu Lys Ile Ser	
107	280 285 290	
109	gag cac ggc ctg ctg acc atc gcc tat caa cgg gaa gga tcc gct	1027
110	Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln Arg Glu Gly Ser Ala	
111	295 300 305	
113	ccg gtc tac gcg ctg gaa ggt tcc gta tcc atg ggc ggt tcc ttg gtg	1075
114	Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met Gly Gly Ser Leu Val	
115	310 315 320 325	
117	cag tgg ctg cgc gac aac cta cag cta atc ccc aac gca cca gcg att	1123
118	Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro Asn Ala Pro Ala Ile	
119	330 335 340	
121	gaa aac ctc gcc cga gaa gtc gaa gac aac ggt ggc gtt cat gtt gtc	1171
122	Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly Gly Val His Val Val	
123	345 350 355	
125	cca gca ttc acc gga ctg ttc gca cca cgt tgg cgc ccc gat gct cgt	1219
126	Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp Arg Pro Asp Ala Arg	
127	360 365 370	
129	ggc gtc att aca ggc ctc acc cgt ttt gcc aac cgc aaa cac atc gcc	1267

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130	Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn Arg Lys His Ile Ala			
131	375	380	385	
133	cgc gca gtc ctt gaa gcc aac gcc ttc caa acc cgc gaa gtt gtg gac	1315		
134	Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr Arg Glu Val Val Asp			
135	390	395	400	405
137	gcc atg gcc aaa gac gca ggc aaa gcc ctc gaa tcc ctc cgc gtc gac	1363		
138	Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Gln Ser Leu Arg Val Asp			
139	410	415	420	
141	ggc gtc atg gtc gaa aat gac ctc ctc atg caa atg caa gcc gac ttc	1411		
142	Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln Met Gln Ala Asp Phe			
143	425	430	435	
145	ctc ggc atc gac gtc caa cgt ctc gag gac gta gaa acc acc gcc gtc	1459		
146	Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val Glu Thr Thr Ala Val			
147	440	445	450	
149	ggc gtc gca ttc gct gca ggt ctc ggc tct gga ttc ttc aaa aca act	1507		
150	Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly Phe Phe Lys Thr Thr			
151	455	460	465	
153	gac gag atc gaa aaa ctt att gca gtg aag aaa gtc tgg aac cct gac	1555		
154	Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys Val Trp Asn Pro Asp			
155	470	475	480	485
157	atg agc gaa gaa gag cgc gaa cgt cgc tat gcc gaa tgg aat agg gca	1603		
158	Met Ser Glu Glu Arg Glu Arg Arg Tyr Ala Glu Trp Asn Arg Ala			
159	490	495	500	
161	gtg gag cat tct tat gac cag gcc tagctgattt gggtcggcct tta	1650		
162	Val Glu His Ser Tyr Asp Gln Ala			
163	505			
166	<210> SEQ ID NO: 2			
167	<211> LENGTH: 509			
168	<212> TYPE: PRT			
169	<213> ORGANISM: Corynebacterium glutamicum			
171	<400> SEQUENCE: 2			
172	Met Arg Ile Ser Lys Ala Asn Ala Tyr Val Ala Ala Ile Asp Gln Gly			
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174	Thr Thr Ser Thr Arg Cys Ile Phe Ile Asp Ala Gln Gly Lys Val Val			
175	20	25	30	
176	Ser Ser Ala Ser Lys Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp			
177	35	40	45	
178	Val Glu His Asp Pro Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val			
179	50	55	60	
180	Ser Gln Ala Met Val Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser			
181	65	70	75	80
182	Leu Gly Val Thr Asn Gln Arg Glu Thr Thr Val Val Trp Asp Lys His			
183	85	90	95	
184	Thr Gly Glu Pro Val Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr			
185	100	105	110	
186	Ser Asp Ile Cys Leu Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp			
187	115	120	125	
188	Leu Asp Arg Thr Gly Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys			
189	130	135	140	

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190 Ile Lys Trp Ile Leu Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu
 191 145 150 155 160
 192 Lys Gly Asp Leu Leu Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn
 193 165 170 175
 194 Leu Thr Gly Gly Val Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val
 195 180 185 190
 196 Thr Asp Val Thr Asn Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr ...
 197 195 200 205
 198 Gln Gln Trp Asp Pro Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser
 199 210 215 220
 200 Met Leu Pro Glu Ile Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg
 201 225 230 235 240
 202 His Arg Gly Thr Leu Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp
 203 245 250 255
 204 Gln Gln Ala Ala Leu Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala
 205 260 265 270
 206 Lys Asn Thr Tyr Gly Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr
 207 275 280 285
 208 Ser Leu Lys Ile Ser Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln
 209 290 295 300
 210 Arg Glu Gly Ser Ala Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met
 211 305 310 315 320
 212 Gly Gly Ser Leu Val Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro
 213 325 330 335
 214 Asn Ala Pro Ala Ile Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly
 215 340 345 350
 216 Gly Val His Val Val Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp
 217 355 360 365
 218 Arg Pro Asp Ala Arg Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn
 219 370 375 380
 220 Arg Lys His Ile Ala Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr
 221 385 390 395 400
 222 Arg Glu Val Val Asp Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu
 223 405 410 415
 224 Ser Leu Arg Val Asp Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln
 225 420 425 430
 226 Met Gln Ala Asp Phe Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val
 227 435 440 445
 228 Glu Thr Thr Ala Val Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly
 229 450 455 460
 230 Phe Phe Lys Thr Thr Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys
 231 465 470 475 480
 232 Val Trp Asn Pro Asp Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala
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 235 500 505
 238 <210> SEQ ID NO: 3
 239 <211> LENGTH: 35
 240 <212> TYPE: DNA

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Input Set : E:\seqlist.txt
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241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Oligonucleotide
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249 <210> SEQ ID NO: 4
250 <211> LENGTH: 34
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: Oligonucleotide
257 <400> SEQUENCE: 4
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260 <210> SEQ ID NO: 5
261 <211> LENGTH: 4323
262 <212> TYPE: DNA
263 <213> ORGANISM: Corynebacterium glutamicum
265 <400> SEQUENCE: 5
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267 tatcgctgac atcgatgctc ttctcgctta attaacaatt gggatccctt agacccggga 120
268 ttaaatcgcc tagcgggctg ottaaaggaag cggAACACGT agaaAGCCAG tccgcagaaa 180
269 cggtgctgac cccggatgaa tgtcagctac tggctatct ggacaaggaa aaacgcaagc 240
270 gcaaaagagaa agcaggttagc ttgcagtggg cttacatggc gatacgatcg ctggcggtt 300
271 ttatggacac caagcgaacc ggaattgcca gctggggcgc cctctggtaa ggttgggaaag 360
272 ccctgcaaaag taaactggat ggctttcttg ccgcggatgaa tctgtatggc caggggatca 420
273 agatctgatc aagagacagg atgaggatcg ttgcatgtt ttaacaaga tggattgcac 480
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275 atcggctgtt ctgatgccgc cgtgttccgg ctgtcagcgc aggggcggcc ggttctttt 600
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279 cctggccgaga aagtatccat catggctgtat gcaatgcgc ggctgcatac gcttgatccg 840
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288 cccggccctt ctatgaaagg ttgggttcgtt gaaatcgatcg ccgggacgccc ggctggatga 1380
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295 aacccgacag gactataaag ataccaggcg tttcccccgtt gaaagctccct cgtgcgtct 1800
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/579,693

DATE: 05/31/2006

TIME: 13:29:05

Input Set : E:\seqlist.txt

Output Set: N:\CRF4\05312006\J579693.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date